

# SEQUENCE LISTING

<110> Deutsches Krebsforschungszentrum

<120> Use of ADAM 12 for diagnosis and therapy of preeclampsia

<130> DK62208PC

<150> EP03023815.8

<151> 2003-10-17

<160> 20

<170> PatentIn version 3.1

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Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp	865		870		875
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636

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agt gca acc aac aga tac aaa ctc ttc cca gcg aag aag ctg aaa agc  
828

Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser  
160 165 170

gtc cgg gga tca tgt gga tca cat cac aac aca cca aac ctc gct gca  
876

Val Arg Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala

175		180		185		190
aag aat gtg ttt cca cca ccc tct cag aca tgg gca aga agg cat aaa						
924						
Lys Asn Val Phe	Pro Pro Pro Ser Gln Thr	Trp Ala Arg Arg His Lys				
	195	200			205	
aga gag acc ctc aag gca act aag tat gtg gag ctg gtg atc gtg gca						
972						
Arg Glu Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala						
	210	215			220	
gac aac cga gag ttt cag agg caa gga aaa gat ctg gaa aaa gtt aag						
1020						
Asp Asn Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys						
	225	230			235	
cag cga tta ata gag att gct aat cac gtt gac aag ttt tac aga cca						
1068						
Gln Arg Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro						
	240	245			250	
ctg aac att cgg atc gtg ttg gta ggc gtg gaa gtg tgg aat gac atg						
1116						
Leu Asn Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met						
	255	260			265	270
gac aaa tgc tct gta agt cag gac cca ttc acc agc ctc cat gaa ttt						
1164						
Asp Lys Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe						
	275	280			285	
ctg gac tgg agg aag atg aag ctt cta cct cgc aaa tcc cat gac aat						
1212						
Leu Asp Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn						
	290	295			300	
gcg cag ctt gtc agt ggg gtt tat ttc caa ggg acc acc atc ggc atg						
1260						
Ala Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met						
	305	310			315	
gcc cca atc atg agc atg tgc acg gca gac cag tct ggg gga att gtc						
1308						
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val						
	320	325			330	
atg gac cat tca gac aat ccc ctt ggt gca gcc gtg acc ctg gca cat						
1356						
Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His						
	335	340			345	350
gag ctg ggc cac aat ttc ggg atg aat cat gac aca ctg gac agg ggc						
1404						
Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly						
	355	360			365	
tgt agc tgt caa atg gcg gtt gag aaa gga ggc tgc atc atg aac gct						
1452						
Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala						
	370	375			380	

tcc acc ggg tac cca ttt ccc atg gtg ttc agc agt tgc agc agg aag  
 1500  
 Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys  
 385 390 395

gac ttg gag acc agc ctg gag aaa gga atg ggg gtg tgc ctg ttt aac  
 1548  
 Asp Leu Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn  
 400 405 410

ctg ccg gaa gtc agg gag tct ttc ggg ggc cag aag tgt ggg aac aga  
 1596  
 Leu Pro Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg  
 415 420 425 430

ttt gtg gaa gaa gga gag gag tgt gac tgt ggg gag cca gag gaa tgt  
 1644  
 Phe Val Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys  
 435 440 445

atg aat cgc tgc tgc aat gcc acc acc tgt acc ctg aag ccg gac gct  
 1692  
 Met Asn Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala  
 450 455 460

gtg tgc gca cat ggg ctg tgc tgt gaa gac tgc cag ctg aag cct gca  
 1740  
 Val Cys Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala  
 465 470 475

gga aca gcg tgc agg gac tcc agc aac tcc tgt gac ctc cca gag ttc  
 1788  
 Gly Thr Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe  
 480 485 490

tgc aca ggg gcc agc cct cac tgc cca gcc aac gtg tac ctg cac gat  
 1836  
 Cys Thr Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp  
 495 500 505 510

ggg cac tca tgt cag gat gtg gac ggc tac tgc tac aat ggc atc tgc  
 1884  
 Gly His Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys  
 515 520 525

cag act cac gag cag cag tgt gtc aca ctc tgg gga cca ggt gct aaa  
 1932  
 Gln Thr His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys  
 530 535 540

cct gcc cct ggg atc tgc ttt gag aga gtc aat tct gca ggt gat cct  
 1980  
 Pro Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro  
 545 550 555

tat ggc aac tgt ggc aaa gtc tcg aag agt tcc ttt gcc aaa tgc gag  
 2028  
 Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu  
 560 565 570

atg aga gat gct aaa tgt gga aaa atc cag tgt caa gga ggt gcc agc  
 2076  
 Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser  
 575 580 585 590  
  
 cgg cca gtc att ggt acc aat gcc gtt tcc ata gaa aca aac atc ccc  
 2124  
 Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro  
 595 600 605  
  
 ctg cag caa gga ggc cgg att ctg tgc cgg ggg acc cac gtg tac ttg  
 2172  
 Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu  
 610 615 620  
  
 ggc gat gac atg ccg gac cca ggg ctt gtg ctt gca ggc aca aag tgt  
 2220  
 Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys  
 625 630 635  
  
 gca gat gga aaa atc tgc ctg aat cgt caa tgt caa aat att agt gtc  
 2268  
 Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val  
 640 645 650  
  
 ttt ggg gtt cac gag tgt gca atg cag tgc cac ggc aga ggg gtg tgc  
 2316  
 Phe Gly Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys  
 655 660 665 670  
  
 aac aac agg aag aac tgc cac tgc gag gcc cac tgg gca cct ccc ttc  
 2364  
 Asn Asn Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe  
 675 680 685  
  
 tgt gac aag ttt ggc ttt gga gga agc aca gac agc ggc ccc atc cgg  
 2412  
 Cys Asp Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg  
 690 695 700  
  
 caa gca gaa gca agg cag gaa gct gca gag tcc aac agg gag cgc ggc  
 2460  
 Gln Ala Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly  
 705 710 715  
  
 cag ggc cag gag ccc gtg gga tcg cag gag cat gcg tct act gcc tca  
 2508  
 Gln Gly Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser  
 720 725 730  
  
 ctg aca ctc atc tga gccctcccat gacatggaga ccgtgaccag tgctgctgca  
 2563  
 Leu Thr Leu Ile  
 735  
  
 gaggaggtca cgcgtcccca aggctcctg tgactggcag cattgactct  
 gtggctttgc 2623  
  
 catcgtttcc atgacaacag acacaacaca gttctcgggg ctcaggaggg  
 gaagtcagc 2683



ctaccaggca ggtctgcaga aacagtgcaa ggaagggcag cgacttcctg  
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 accactctgg 2803  
  
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 gcagtactca 3163  
  
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 catttaacaa 3223  
  
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<210> 4

<211> 738

<212> PRT

<213> Homo sapiens

<400> 4

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Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	Val	Ser
			20					25					30		

Leu	Trp	Asn	Glu	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	Ser	Val	Arg
		35					40					45			

Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	Ser	Lys	Asn	His
	50					55					60				

Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile  
 65 70 75 80

Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu  
 85 90 95

Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr  
 100 105 110

Thr Val Ile Leu Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr  
 115 120 125

Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu  
 130 135 140

Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala  
 145 150 155 160

Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg  
 165 170 175

Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn  
 180 185 190

Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu  
 195 200 205

Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn  
 210 215 220

Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg  
 225 230 235 240

Leu Ile Glu Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn  
 245 250 255

Ile Arg Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys  
 260 265 270

Cys Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp  
 275 280 285

Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala Gln  
 290 295 300

Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met Ala Pro  
 305 310 315 320

Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile Val Met Asp  
 325 330 335

His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu Ala His Glu Leu  
 340 345 350

Gly His Asn Phe Gly Met Asn His Asp Thr Leu Asp Arg Gly Cys Ser  
 355 360 365

Cys Gln Met Ala Val Glu Lys Gly Gly Cys Ile Met Asn Ala Ser Thr  
 370 375 380

Gly Tyr Pro Phe Pro Met Val Phe Ser Ser Cys Ser Arg Lys Asp Leu  
 385 390 395 400

Glu Thr Ser Leu Glu Lys Gly Met Gly Val Cys Leu Phe Asn Leu Pro  
 405 410 415

Glu Val Arg Glu Ser Phe Gly Gly Gln Lys Cys Gly Asn Arg Phe Val  
 420 425 430

Glu Glu Gly Glu Glu Cys Asp Cys Gly Glu Pro Glu Glu Cys Met Asn  
 435 440 445

Arg Cys Cys Asn Ala Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys  
 450 455 460

Ala His Gly Leu Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr  
 465 470 475 480

Ala Cys Arg Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr  
 485 490 495

Gly Ala Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His  
 500 505 510

Ser Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr  
 515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro Ala  
 530 535 540

Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro Tyr Gly

545		550		555		560
Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys Glu Met Arg						
	565			570		575
Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly Ala Ser Arg Pro						
	580		585		590	
Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr Asn Ile Pro Leu Gln						
	595		600		605	
Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr His Val Tyr Leu Gly Asp						
	610		615		620	
Asp Met Pro Asp Pro Gly Leu Val Leu Ala Gly Thr Lys Cys Ala Asp						
	625		630		635	640
Gly Lys Ile Cys Leu Asn Arg Gln Cys Gln Asn Ile Ser Val Phe Gly						
		645		650		655
Val His Glu Cys Ala Met Gln Cys His Gly Arg Gly Val Cys Asn Asn						
	660		665		670	
Arg Lys Asn Cys His Cys Glu Ala His Trp Ala Pro Pro Phe Cys Asp						
	675		680		685	
Lys Phe Gly Phe Gly Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala						
	690		695		700	
Glu Ala Arg Gln Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly						
	705		710		715	720
Gln Glu Pro Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr						
		725		730		735

Leu Ile

<210> 5

<211> 2642

<212> DNA

<213> Homo sapiens

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 ctgccggatt 60  
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 agaagaccac 120  
 cattgaaaaa ctaagggtgtg tgcgcccttc ccggccaccc cgtggcttcc  
 aaccctgtca 180  
 ggctcacctc ggccaccttg gaaaaggcct gatgaggaag ccgccagatt  
 cctaccaccc 240  
 gaaggacaat cccaggagat tgctgcagtg tcagaatggt gacatcagca  
 gaccctcaa 300  
 cggcctgaat gtccttcagc cccagtcaac tcagcgagtg cttcctcccc  
 tccaccgggc 360  
 cccacgtgca cctagcgtcc ctgccagacc cctgccagcc aagcctgcac  
 ttaggcaggc 420  
 ccaggggacc tgtaagcaa accccctca gaagcctctg cctgcagatc  
 ctctggccag 480  
 aacaactcgg ctcactcatg ccttggccag gaccccagga caatgggaga  
 ctgggtccg 540  
 cctggcacc ctcagacctg ctccacaata tccacaccaa gtgcccagat  
 ccaccacac 600  
 cgcctatatt aagtgagaag ccgacacctt ttttcaacag tgaagacaga  
 agtttgact 660  
 atctttcagc tccagttgga gttttttgta ccaactttta ggattttttt  
 taatgttta 720  
 aacatcatta ctataagaac tttgagctac tgccgtcagt gctgtgctgt  
 gctatgggtg 780  
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 gattacagt 840  
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 ggacaggatg 960  
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 aggtgtagcc 1260

acaccaggat agagactgga acactagaca agccagaact tgaccctgag  
 ctgaccagcc 1320

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 atttagcttg 1440

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 ccacctccct 1500

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caacctacct gttgagcatc acagaatgtg ataaggaaat caacttgctt  
 atcaacttcc 1920

taaatattat gagatgtggc ttgggcagca tccccttgaa ctcttcactc  
 ttcaaagccc 1980

tgactaggga gccatgtttc acaagggtctt taaagtgact aatggcatga  
 gaaatacaaa 2040

aatactcaga taaggtaaaa tgccatgatg cctctgtctt ctggactggg  
 tttcacatta 2100

gaagacaatt gacaacagtt acataattca ctctgagtgt tttatgagaa  
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tggggctaac agttttccta tgctttgaaa cagaaaaata tgtaccaaga  
 atcttggttt 2220

gccttccaga aaacaaaact gcatttcaact tccccgggtg tccccactgt  
 atctaggcaa 2280

catagtattc atgactatgg ataaactaaa cacgtgacac aaacacacac  
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 gttattaagt 2400

tctttaaaat gtaaagccat gctggaaaat aatactgctg agatacatat  
agaattactg 2460

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taaaaagggtt 2520

tacagaatgtt tatgggtgcat tacgtgggca ttgtcttttt agatgcccaa  
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aaaaaaaaaa 2640

aa  
2642

<210> 6

<211> 205

<212> PRT

<213> Homo sapiens

<400> 6

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20 25 30

Leu Leu Phe Thr Asn Lys Lys Thr Thr Ile Glu Lys Leu Arg Cys Val  
35 40 45

Arg Pro Ser Arg Pro Pro Arg Gly Phe Gln Pro Cys Gln Ala His Leu  
50 55 60

Gly His Leu Gly Lys Gly Leu Met Arg Lys Pro Pro Asp Ser Tyr Pro  
65 70 75 80

Pro Lys Asp Asn Pro Arg Arg Leu Leu Gln Cys Gln Asn Val Asp Ile  
85 90 95

Ser Arg Pro Leu Asn Gly Leu Asn Val Pro Gln Pro Gln Ser Thr Gln  
100 105 110

Arg Val Leu Pro Pro Leu His Arg Ala Pro Arg Ala Pro Ser Val Pro  
115 120 125

Ala Arg Pro Leu Pro Ala Lys Pro Ala Leu Arg Gln Ala Gln Gly Thr

130	135	140
Cys Lys Pro Asn Pro Pro Gln Lys Pro Leu Pro Ala Asp Pro Leu Ala		
145	150	155 160
Arg Thr Thr Arg Leu Thr His Ala Leu Ala Arg Thr Pro Gly Gln Trp		
	165	170 175
Glu Thr Gly Leu Arg Leu Ala Pro Leu Arg Pro Ala Pro Gln Tyr Pro		
	180	185 190
His Gln Val Pro Arg Ser Thr His Thr Ala Tyr Ile Lys		
	195	200 205

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<211> 908

<212> DNA

<213> Homo sapiens

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catgacatgg 120

agaccgtgac cagtgtgtgt gcagaggagg tcacgcgtcc ccaaggcctc  
ctgtgactgg 180

cagcattgac tctgtggctt tgccatcggt tccatgacaa cagacacaac  
acagttctcg 240

gggctcagga ggggaagtcc agcctaccag gcagggtctgc agaaacagtg  
caaggaaggg 300

cagcgacttc ctggttgagc ttctgctaaa acatggacat gcttcagtgc  
tgctcctgag 360

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agaggactca 420

aaagtctggc ctttcactga gcctccacag cagtggggga gaagcaaggg  
ttgggcccag 480

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ctctggctgc 540

aacttaatgc tctgatatgg cttttagcat ttattatatg aaaatagcag  
ggttttagtt 600



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tgaatggcat 660

tgaaacaaac tggagaagaa ggtaggagaa agggcggtga actctggctc  
tttgctgtgg 720

acatgcgtga ccagcagtac tcaggtttga gggtttgcag aaagccaggg  
aaccacaga 780

gtcaccaacc cttcatttaa caagtaagaa tgttaaaaag tgaaaacaat  
gtaagagcct 840

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ataaaaaaaaa 900

aaaaaaaa  
908

<210> 8

<211> 34

<212> PRT

<213> Homo sapiens

<400> 8

Glu	Ala	Arg	Gln	Glu	Ala	Ala	Glu	Ser	Asn	Arg	Glu	Arg	Gly	Gln	Gly
1				5				10					15		

Gln	Glu	Pro	Val	Gly	Ser	Gln	Glu	His	Ala	Ser	Thr	Ala	Ser	Leu	Thr
			20					25					30		

Leu Ile

<210> 9

<211> 23

<212> DNA

<213> Homo sapiens

<400> 9

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23

<210> 10

<211> 23

<212> DNA

<213> Homo sapiens

<400> 10

gaattcctat ggtaaaccct tgg  
23

<210> 11

<211> 24

<212> DNA

<213> Homo sapiens

<400> 11

cttgctgccg gatttgtggt ttat  
24

<210> 12

<211> 24

<212> DNA

<213> Homo sapiens

<400> 12

agttgactgg ggctgagggga catt  
24

<210> 13

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (15)..(15)

<223> Mismatch (g instead of c)

<400> 13  
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23

<210> 14

<211> 23

<212> DNA

<213> Homo sapiens

<400> 14  
ggactctgca gcttcctgcc ttg  
23

<210> 15

<211> 21

<212> DNA

<213> Homo sapiens

<400> 15  
tcggggctca ggaggggaag t  
21

<210> 16

<211> 21

<212> DNA

<213> Homo sapiens

<400> 16  
ggctgccaag gcggaggtgt c  
21

<210> 17

<211> 24

<212> DNA

<213> Homo sapiens

<400> 17  
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24

<210> 18

<211> 24

<212> DNA

<213> Homo sapiens

<400> 18  
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24

<210> 19

<211> 21

<212> DNA

<213> Homo sapiens

<400> 19  
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21

<210> 20

<211> 21

<212> DNA

<213> Homo sapiens

<400> 20  
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21